



**FIG. 1**

PF4 (SEQ ID NO:2) : <sup>47</sup>NGRRICLDLQAPLYKKIIKKLLES<sup>70</sup>  
IL-8 (SEQ ID NO:3) : <sup>46</sup>GRELCCLDPKENWVQRVVEKFLKRAENS<sup>72</sup>  
ATIII (SEQ ID NO:4) : <sup>118</sup>QIHFFFAKLNCRLYRKANKSSKLVSANRLFGDKS<sup>151</sup>  
ApoE (SEQ ID NO:5) : <sup>132</sup>ELRVRLASHLRKLRKRLLRDADDLQKRLAVYQAG<sup>165</sup>  
AAMP (SEQ ID NO:6) : <sup>14</sup>RRLRRMESESES<sup>25</sup>  
Ampiregulin (SEQ ID NO:7) : <sup>25</sup>KRKKKGGKNGKNTTNTKKKNP<sup>45</sup>

**FIG. 2**

NEU2 (SEQ ID NO:8): 1 MASLPVLQKE SVFQSGAHA- -YRIPALLYL PGQQSLLAFA EQRASKKDEH  
 YR+P+LL + P +LLAF EQR S D H  
 NEU4 (SEQ ID NO:9): 1 MGVPRTPSRT VLFERERTGL TYRVPSLLPV PPGPTLLAFV EQRLSPDDSH

NEU2: 49 AELIVLRRGD YDAPTHQVQW QAQEVVAQAR LDGHRSMNPC PLYDAQTGTL FLFFIAIPGQ  
 A +VLRRG +W A ++ A HRSMNPC P++DA TGT+ FLFFIA+ G  
 NEU4: 51 AHRLVLRRGT LAGGSV--RW GALHVLGTAA LAEHRSMNPC PVHDAGTGTV FLFFIAVLGH

NEU2: 110 VTEQQQLQTR ANVTRLCQVT STDHGRTWSS PRDLTDAAIG PAYREWSTFA VGPGHCLQLN  
 E Q+ T N RLC V S D G +W S RDLT+ AIG A ++W+TFA VGPGH +QL  
 NEU4: 109 TPEAVQIATG RNAARLCCVA SRDAGLSWGS ARDLTEEAIG GAVQDWATFA VGPGHGVQLP

NEU2: 170 DRARSLVVPA YAYRKLHP-- ---IQRPIPS AFCFLSHDHG RTWARGHFVA QD-TLECQVA  
 R L+VPA Y YR I R P +F F S DHG RTW G V + ECQ+A  
 NEU4: 169 S-GR-LLVPA YTYRVDRLEC FGKICRTSPH SFAFYSDDHG RTWRCGGLVP NLRSGECQLA

NEU2: 224 EVETGEQRVV TL-NARSHLR ARVQAQSTND GLDFQESQLV KKLVEPPPQG CQGSVISFPS  
 V+ G+ NARS L +RVQA ST++ G F ++ V L E G CQGS++ FP  
 NEU4: 227 AVDGGQAGSF LYCNARSPLG SRVQALSTDE GTSFLPAERV ASLPETAW-G CQGSIVGFPA

NEU2: 283 P-----

NEU4: 286 PAPNRPRDDS WSVGPRSPLO PPLLGPVHE PPEEAAVDPR GGQVPGGPFS RLQPRGDGP

NEU2: 284 ----- ---RSGPGSP QWLLYTHPTH SWQRADLGAY LNPRPPAPEA  
 WLLY+HP R +G L+ P P +  
 NEU4: 346 RQPGPRPGVSG DVGSWTLALP MPFAAPPQSP TWLLYSHPVG RRARLHMGIR LSQSPLDPRS

NEU2: 321 WSEPVLLAKG SCAYSDLQSM GTGPDGSPLF GCLYEANDY- --EEIVFLMF TLKQAFPAEY  
 W+EP ++ + YSDL S+ G P+G +F +CLYE +L++  
 NEU4: 406 WTEPWVIYEG PSGYSDLASI GPAPEGGLVF ACLYESGART SYDEISFCTF SLREVLENVP

NEU2: 378 LPQ

NEU4: 466 ASPKPPNLGD KPRGCCWPS

**FIG. 3**

Substrate Specificity of Bacteria and Fungal Sialidases

Substrates	Sialidase activity*					
	Vibrio Cholerae	Clostridium perfringens (71Kd)	Clostridium perfringens (43Kd)	Arthrobacter ureafaciens	Salmonella typhimurium	Actinomyces viscosus
Oligo- and polysaccharides						
II <sup>3</sup> Neu5AcLac	100	100	100	100	100	100
II <sup>6</sup> Neu5AcLac	53	44	19	157	0.4	462
Colominic acid (α2-8)	30	33	4.0	63	0.1	300
Glycoproteins						
Fetuin (α2-3>α2-6)	340	272	6.6	59	17	---
α1-Acid glycoprotein (α2-6>α2-3)	1000	555	---	---	---	761
Submandibular gland mucin (α2-6)	400	139	5.1	---	---	123
Submaxillary gland mucin (α2-6)	---	---	---	56	---	---
Gangliosides						
Gangliosides mixtures Synthetic	(360)	(350)	1.6	78	34	285
4MU-Neu5Ac	1580	605	58	---	1050	---

\* Each value represents a relative sialidase activity when the activity directed toward II<sup>3</sup>Neu5AcLac is regard as 100.

FIG.4